



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/502,498C

DATE: 01/21/2004

TIME: 15:08:56

Input Set : A:\seq list 09502498.txt

Output Set: N:\CRF4\01202004\I502498C.raw

3 <110> APPLICANT: Kilian, Andrzej  
 4 Bowtell, David  
 6 <120> TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES  
 7 THEREOF  
 9 <130> FILE REFERENCE: 407C2  
 11 <140> CURRENT APPLICATION NUMBER: 09/502,498C  
 12 <141> CURRENT FILING DATE: 2000-02-11  
 15 <160> NUMBER OF SEQ ID NOS: 155  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 3964  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <400> SEQUENCE: 1

P.6

ENTERED

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 27 cgcggggacc cggcggttt ccgcgcgtg gtggccagt gcctggtgtg cgtgccctgg 180  
 28 gacgcacggc cgcceccgc cgccccctcc ttccgccagg tgctctgcct gaaggagctg 240  
 29 gtggcccgag tgctgcagag gctgtgcgag cgcggcgca agaactgtct ggccctcggc 300  
 30 ttccgcgtgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360  
 31 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcggt ggggctgctg 420  
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55 tggagcaagt tgcaaagcat tggaaatcaga cagcacttga agaggggtgca gctgcgggag 1800
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57 ctccgcttca tccccaaagcc tgacgggctg cgcccgattg tgaacatgga ctacgtcgtg 1920
58 ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
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90 gtgtgccctg tacacaggcg aggacctgc acctggatgg gggtcctgt ggggtcaaat 3900
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94 &lt;210&gt; SEQ ID NO: 2

95 &lt;211&gt; LENGTH: 1132

96 &lt;212&gt; TYPE: PRT

97 &lt;213&gt; ORGANISM: Homo sapiens

99 &lt;400&gt; SEQUENCE: 2

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101   1               5               10               15
103 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
104           20           25           30
106 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
107           35           40           45

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109 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
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113 65                      70                      75                      80
115 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
116      85                      90                      95
118 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
119      100                     105                     110
121 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
122      115                     120                     125
124 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
125      130                     135                     140
127 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
128 145                      150                      155                      160
130 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
131      165                      170                      175
133 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
134      180                      185                      190
136 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
137      195                      200                      205
139 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
140      210                     215                     220
142 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
143 225                      230                      235                      240
145 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
146      245                      250                      255
148 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
149      260                     265                     270
151 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
152      275                     280                     285
154 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
155      290                     295                     300
157 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
158 305                      310                      315                      320
160 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
161      325                      330                      335
163 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
164      340                     345                     350
166 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
167      355                     360                     365
169 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
170      370                     375                     380
172 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
173 385                      390                      395                      400
175 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
176      405                     410                     415
178 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
180      420                     425                     430
182 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu

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185 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
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188 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
189 465          470          475          480
191 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
192          485          490          495
194 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
195          500          505          510
197 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
198          515          520          525
200 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
201          530          535          540
203 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
204 545          550          555          560
206 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
207          565          570          575
209 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
210          580          585          590
212 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
213          595          600          605
215 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
216          610          615          620
218 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
219 625          630          635          640
221 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
222          645          650          655
224 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
225          660          665          670
227 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
228          675          680          685
230 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
231          690          695          700
233 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
234 705          710          715          720
236 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
237          725          730          735
239 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
240          740          745          750
242 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
243          755          760          765
245 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
246          770          775          780
248 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
249 785          790          795          800
251 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
252          805          810          815
254 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
255          820          825          830

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260 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
261      850      855      860
263 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
264 865      870      875      880
266 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
267      885      890      895
269 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
270      900      905      910
272 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
273      915      920      925
275 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
276      930      935      940
278 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
279 945      950      955      960
281 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
282      965      970      975
284 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
285      980      985      990
287 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln
288      995      1000      1005
290 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
291      1010      1015      1020
293 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
294 1025      1030      1035      1040
296 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
297      1045      1050      1055
299 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
300      1060      1065      1070
302 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
303      1075      1080      1085
305 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
306      1090      1095      1100
308 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
309 1105      1110      1115      1120
311 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
312      1125      1130
315 <210> SEQ ID NO: 3
316 <211> LENGTH: 1031
317 <212> TYPE: PRT
318 <213> ORGANISM: Euplotes aediculatus
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325      20      25      30
327 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
328      35      40      45

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 1,2,3,4,5,6,7  
Seq#:34; N Pos. 1767,1768,1769  
Seq#:51; N Pos. 1871,1872,1873  
Seq#:91; Xaa Pos. 2,3,4,5  
Seq#:93; Xaa Pos. 2,3,4,5,7,8  
Seq#:95; N Pos. 1,2,3,5,9,10,11,12,13,14